

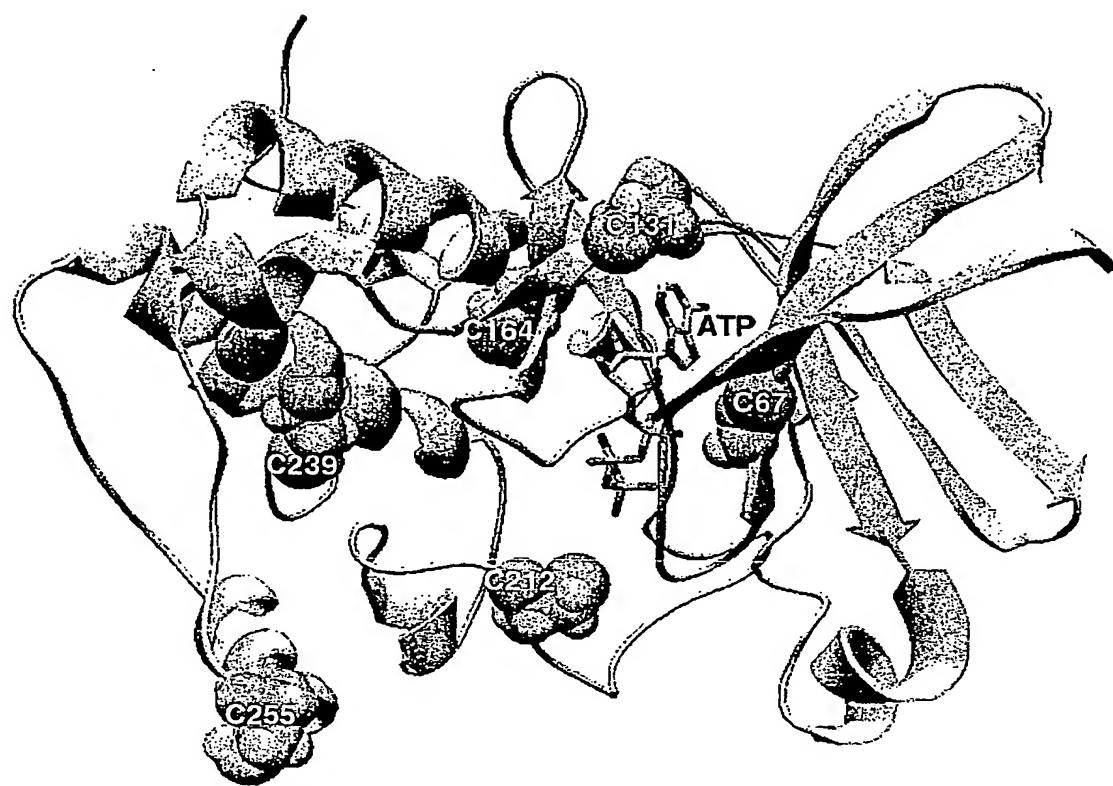
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sp	P53350	-----MS-AAVTAGKLARA-----PADPGKAGVPGVAAPG---APAAAP
sp	Q9NYY3	MELLRTITYQPAASTKMCSEQALGKGCGADSKKRPPQPPPEESQPPQSQAQVPPAAPHHHH
sp	Q9H4B4	-----MEPAAG-FLSPRPFQRTAAATA---PPAGPG---PPPSALRGPELEMLAGL
	 * : * * * * *
sp	P53350	PAKEIP---EVLVDPRSRRLRYVRGRFLGKGFFAKCFEISDADTKEVFAGKIVPKSLLLK
sp	Q9NYY3	HHSHSGPEISRIIVDPTGKRYCRGKVLGKGFFAKCYEMDTLNKVKYAAKIIIPHSRVAK
sp	Q9H4B4	PTSDPG---RLITDPRSGRTYLGKRLLGKGFFARCYEATDTETGSAYAVKVIPOSRVVK
	:.* : : * : : .:*****: * : * . .: * * : * : * : *
sp	P53350	PHQREKMSMEISIHRSLAHQHVVGFFHGFEDNDFVFWLELCRRRSILLEHKRRKALTEP
sp	Q9NYY3	PHQREKIDKEIELHRLHHKHVVQFYHYFEDKENIYILLEYCSRRSMAHILKARKVLTEP
sp	Q9H4B4	PHQREKILNEIELHRLQHHRHIVRFSHHFEDADNIYIIFLECSRKSLSLAHIWKARHTLLEP
		*****: * .:*** * * : * .*** : : .:*** * * : * : .: * * : * ***
sp	P53350	EARYYLQIVLGCQYLHNRNRVIHDLKLGNLFLNEDLEVKGIDGFLATKVEYDGERKTL
sp	Q9NYY3	EVRYYLQIVSGLKYLHQEILHRLKLGNFFINEAMELKVGDFGLAARLEPLEHRRRTI
sp	Q9H4B4	EVRYYLQILSGLKYLHORGILHRLKLGNFFITENMELKVGDFGLAARLEPPEQRKKTI
		*.*****: * :**** .:*****: * : .:*****: * : * :*****: * .:***:
sp	P53350	CGTPNYIAPEVLSKKGHSFEVDVWSIGCIMYTLLVGKPFETSLKETYLRKKNEYSIP
sp	Q9NYY3	CGTPNYLSPEVLSNKQGHGCESDIWALGCVMYTMLLGRPFETTNLKETYRCIREARYTMP
sp	Q9H4B4	CGTPNYVAPEVLLRQGHGPEADVWSLGCVMYTLLCGSPPFETADLKETYRCIKQVHYTLP
		*****: * :*** .:*** * :***: * : * .:*****: * :***** * : .:***:
sp	P53350	KHINPVAASLIQKMLQTDPPTARPTINELLNDEFFTSGYIIPARLPIT-CLTIP-----PR
sp	Q9NYY3	SSLLAPAKHLIASMLSKNPDRPSLDDIIRHDFLQGFTPDRLSSSCCHTVPDFHLSSPA
sp	Q9H4B4	ASLSPARQLLAIRLASPRDRPSIDQILRHDFFTKGYTPDRLPISSCVTPDLPNPA
		: * * : * . * * : * : .:***** .: * * .: * : * : * : * : *
sp	P53350	--FSIAPSSLDPNSNRK-----P---LTVLNKGLENP---LPER-----
sp	Q9NYY3	KNFFKKAAAALFGGKKDKARYIDTHNRVSKEDEDIYKLRHDLKKTSITQOPSKHRTDEEL
sp	Q9H4B4	RSLFAVTKSLFVRKKK-----SKNHAQERDE-VSGLVSGLMRTSVGHQDAR-----
		* .. : * : .: * .: * .: * .. : * .: * .. : * : .: * : *
sp	P53350	--PRE---KEEPVVR-ET-----GEVVDCHLSDMLQQLHGSVNAKPSERGLVR
sp	Q9NYY3	QPPTTVARSGTPAVENKQQIGDAIRMIVRGTLGSCSSSECLEDSTMGSVADTVARVLR
sp	Q9H4B4	--PEAPAASGPAPVSLVETAPEDSS---PRGTLASSGHG---FEEGLTVATVVESALCALR
		* .. : * .: * .: * .: * .: * .: * .: * .: * .: * .: * .: *
sp	P53350	--QEEAEDPACIP-----IFWVSKWVDYSKDYGLGYQLCDNSVGVLFNDSTRLILYN
sp	Q9NYY3	GCLENMPEADCIKPQLSTS-FQWVTKWVDYSNKYGFYQLSDHTVGVLFNNGAHMSLLP
sp	Q9H4B4	NCIAFMPPAEQNPNPLAQPEPLVWFSEWVGFNSKFGFGYQLSSRRVAVLFNDGTHMALS
		* .. : * .: * .: * .: * .: * .: * .: * .: * .: * .: * .: *
sp	P53350	DGDSLQYIERDGTESYLTVSSHPNSLMKKITLLKFRNYSMEHLLKAGANITPREGDELA
sp	Q9NYY3	DKKTVHYYAELGQCSVFPATDAPEQFISQVTVLKYFSHYMEENLMDGG-DLPSVTDIRR
sp	Q9H4B4	NRKTVHYNPTSTKHFSFSGAVRRALQPOQLGILRYFASYMEQHLMKGG-DLPSVEEVEVP
		: .. : * .. : .. : : * : * : * .. : * : * : * .. : .. : ..
sp	P53350	RLPYLRTWFRTRSAIILHLSNGSVQINFFQDHTKLILCP--LMAAVTYIDEKRDFTTYRL
sp	Q9NYY3	R-LYLLQWLKSDKALMMLFNDGTFQVNFYHDHTKIIICSONEEYLLTYINEDRISTTFR
sp	Q9H4B4	APPLLLQWVKTQDQALLMLFSDGTVQVNFYGDHTKLILSG-WEPLLVTFVARNRSACTYLA
		* .. : . * : .. : .. : * : * .. : * .. : .. : .. : .. : ..
sp	P53350	SLLEBEYGCCKELASRLRYARTMVDKLLSSRSASNRLKAS
sp	Q9NYY3	TTLLMSGCSSELKNRMEYA---LNMLLQRCN-----
sp	Q9H4B4	SHLRQLGCSPLDRQRLRYA---LRLRDRSPA-----
		: * .. : * .. : * .. : * .. : * .. : * .. : * ..

FIGURE 1

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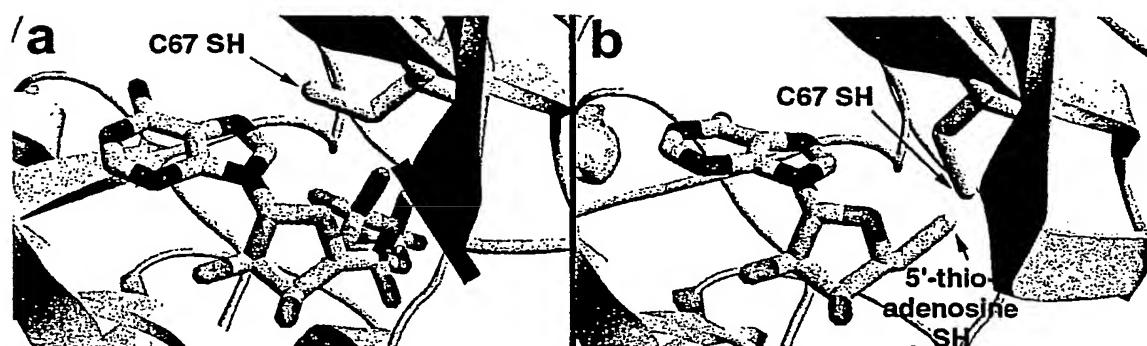
**FIGURE 2**

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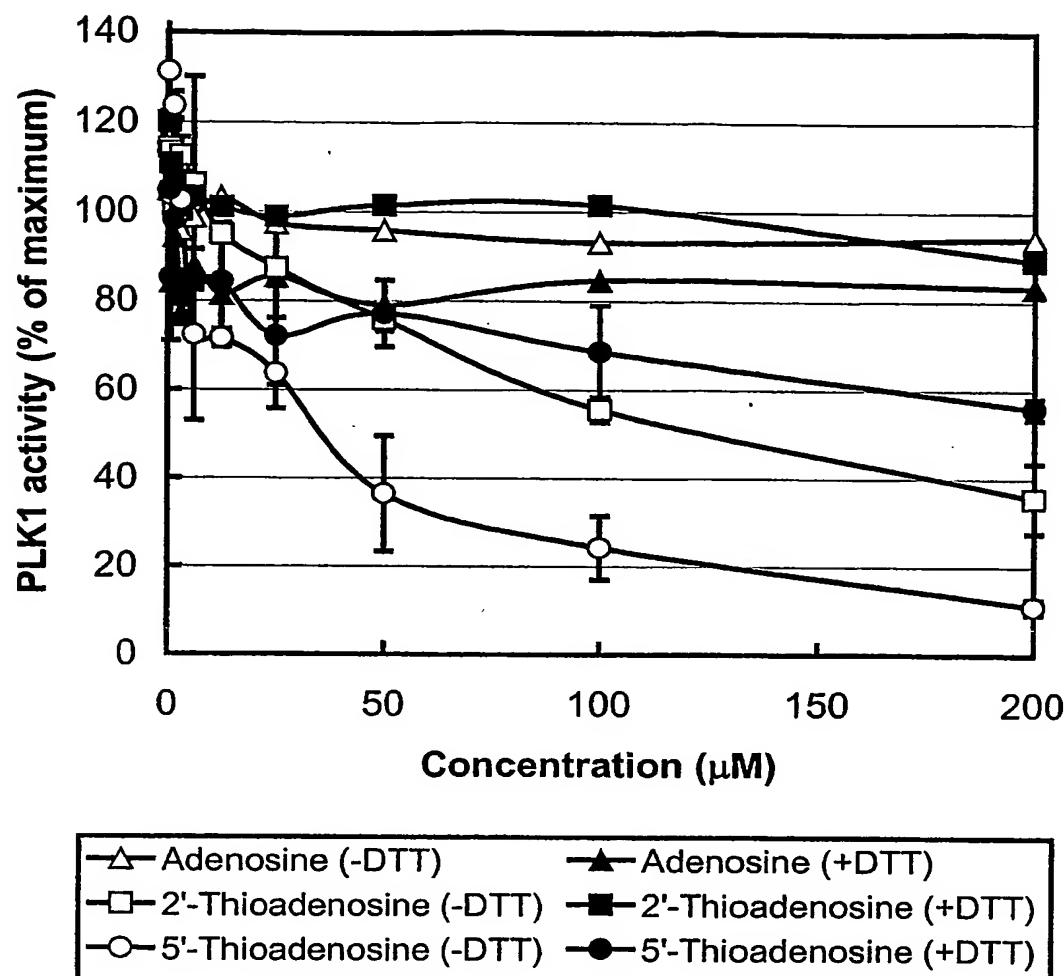
1	MSAAVTAGKLARAPADPGKAGVPGVAAPGAPAAAPPKE---IPEVLVDP 1 1 MGNAAAACKGSEQESVKEFLAKA	47	PLK1 23 PKA
48	RS-----RRRYVRGRFLGKGGFAKC FE ISDADTKEVFACK 24 24 KEDFLKKWESPAQNTAHLDQFERIKTLGIGSFGRVMLVKHKEIGNHYAMK	82	PLK1 73 PKA
83	IVPKSLLLKPHOREKMSMEISIHRSLAHQHVVGFHGFEDNDFVVFVLEL 74 74 ILEKQKVVKLQTEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMMVEY	132	PLK1 123 PKA
133	<u>C</u> RRRSLLLELHKRRKALTEPEARYYL RQ IVL G QYLHRRN R VI H RD L KLGNL 124 124 VPGGEMF S HLRRIGRFSEPARFYAAQ Q IVL T FEYLH S LD L YRDLK P ENL	182	PLK1 173 PKA
183	FLNEDLEV K IGDFGLATKVEYDGER K TLG T PNYIAPEV L SKK G H S FEV 174 174 LIDQQGYIQV T DFGFAKRVK---G R I W TL G TPEYLAPE I ILSKGYNKAV	232	PLK1 220 PKA
233	DVWSIGCIMY T LLVGKPPFET S CLKETYL R IKKNEY S IPK H INPVAASLI 221 221 DW W ALGV L IYEMAAGYPPFFADQ P IQ I YEKIVSGKVR F PSH F SSDLKD L	282	PLK1 270 PKA
283	QKMLQTDPTAR----PTINELLNDEFF-TSGYIPARLPITCLTIPPRFS 271 271 RNLLQVDL T KRFGNLKNGVNDIKNHWFATTDWIAIYQ R KVEAPF I PKFK	326	PLK1 320 PKA

FIGURE 3

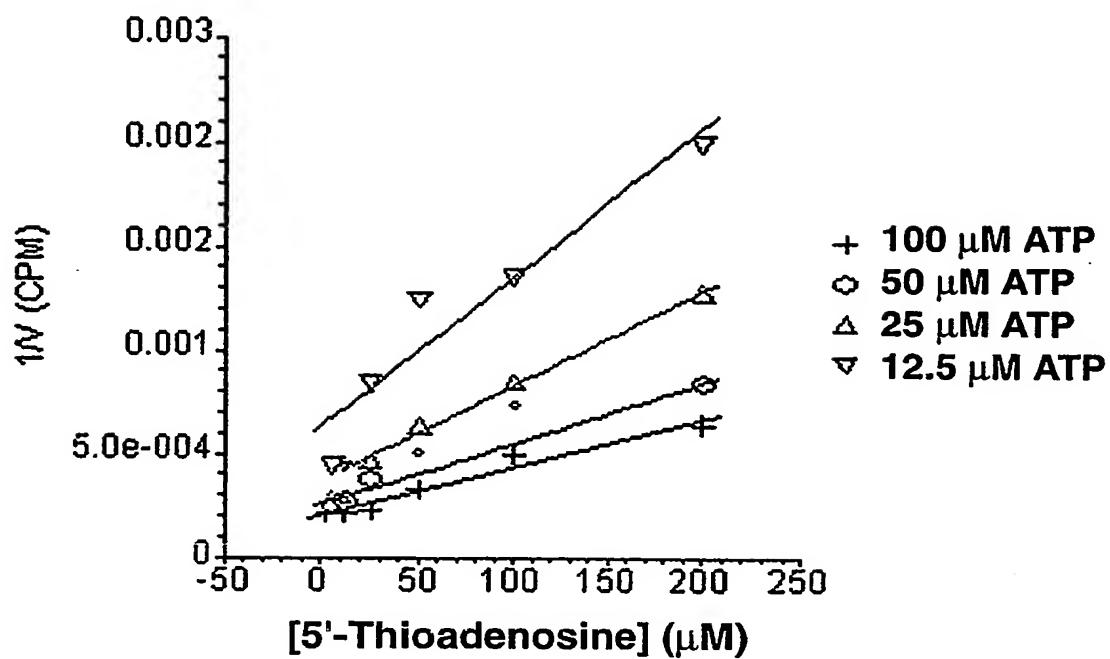
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**FIGURE 4**

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**FIGURE 5**

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**FIGURE 6**

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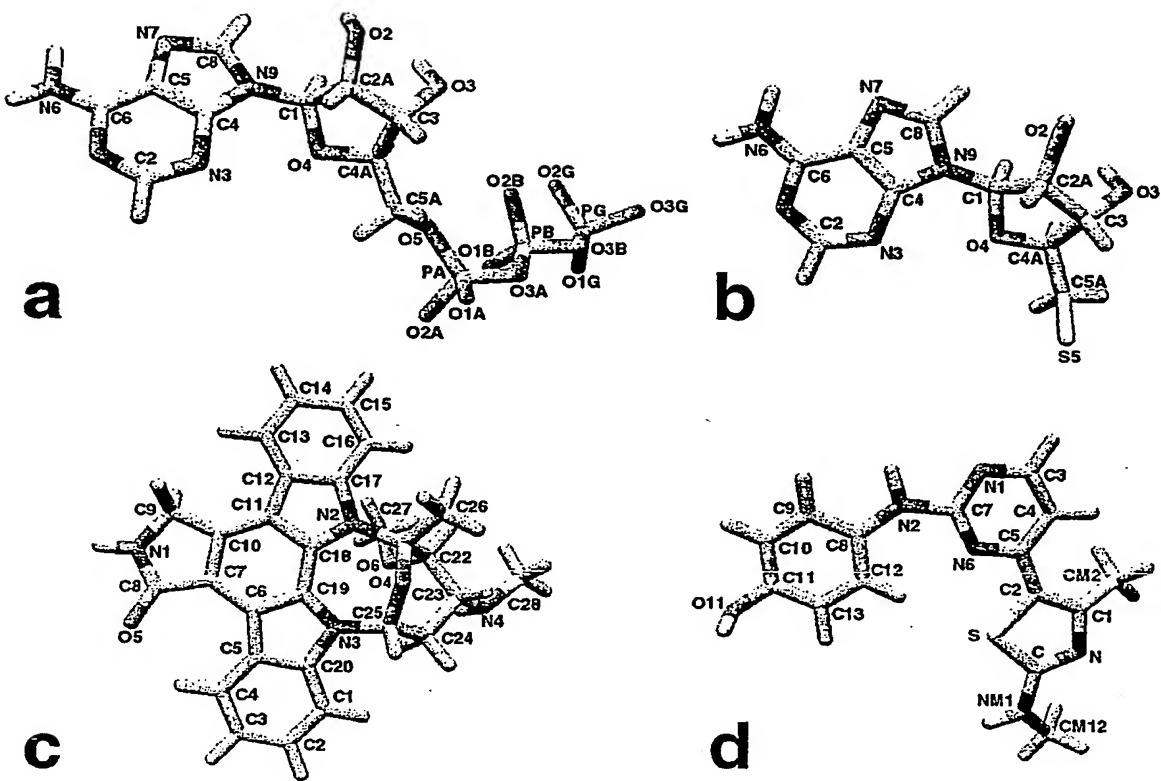


FIGURE 7

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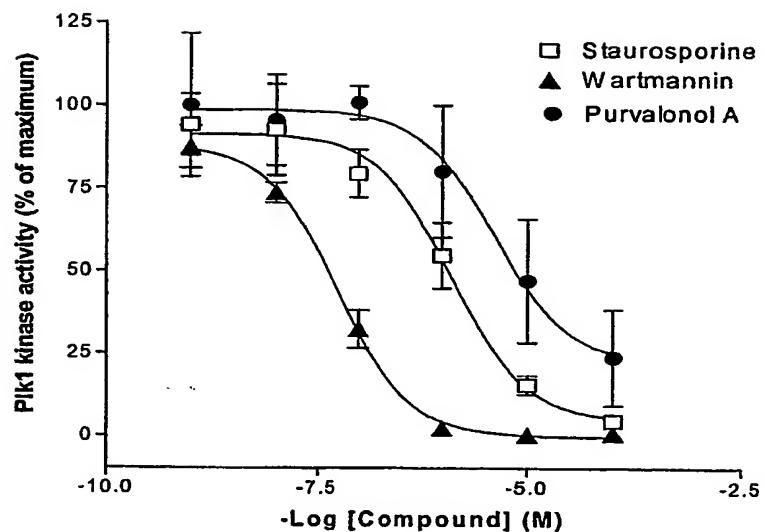


FIGURE 8

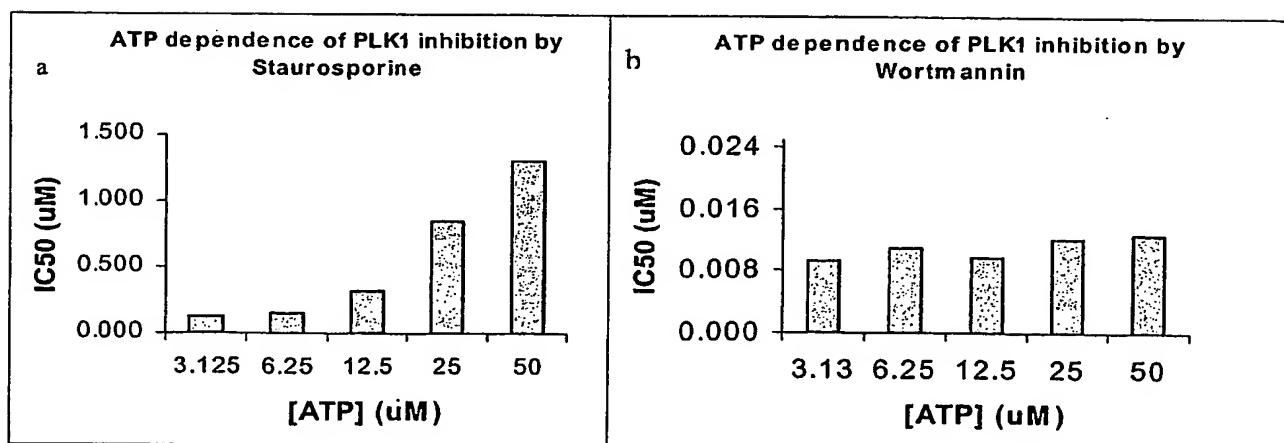


FIGURE 9

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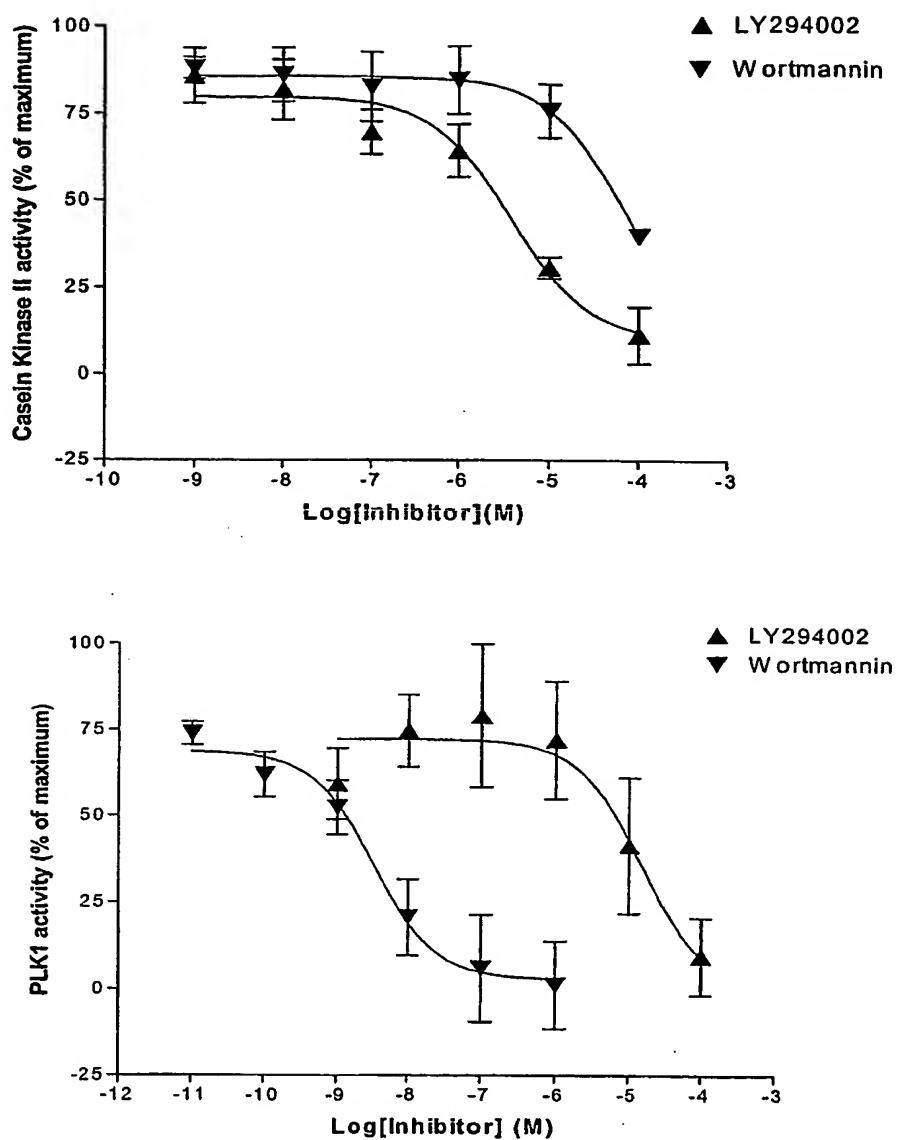
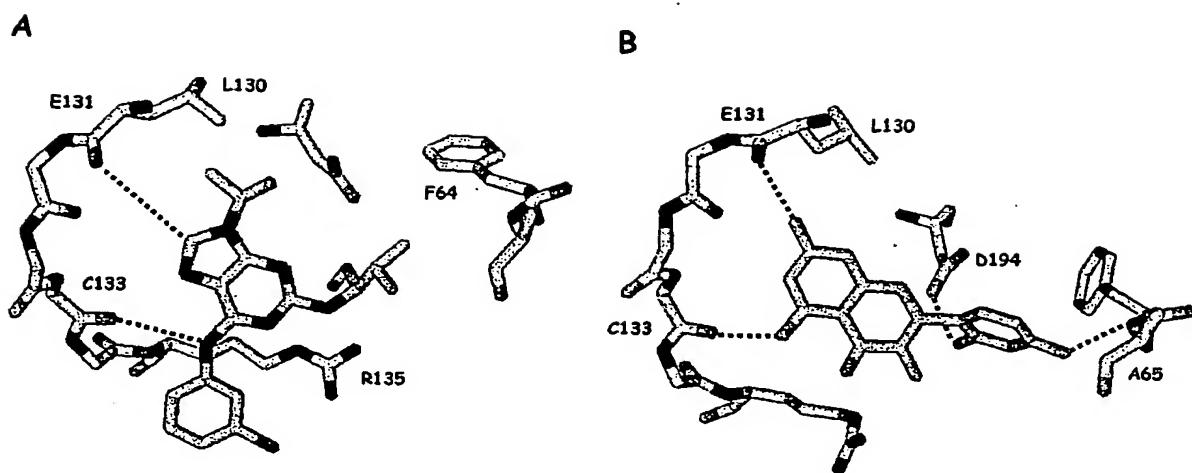
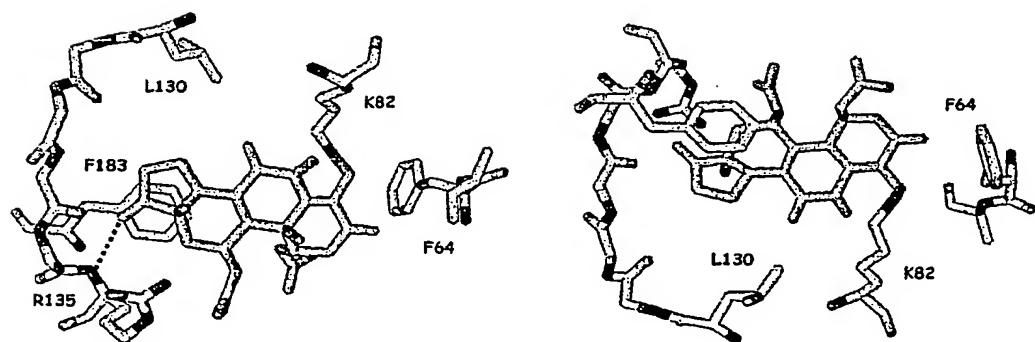


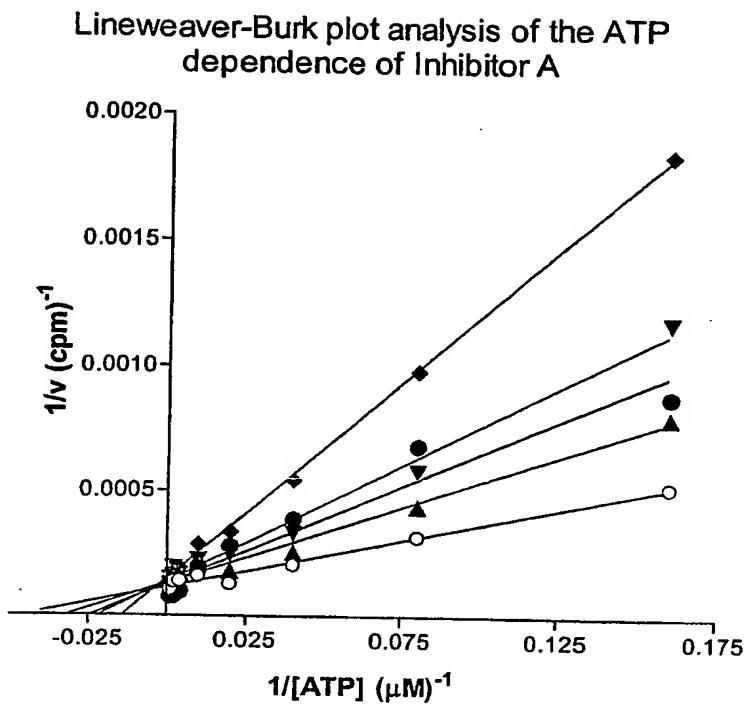
FIGURE 10

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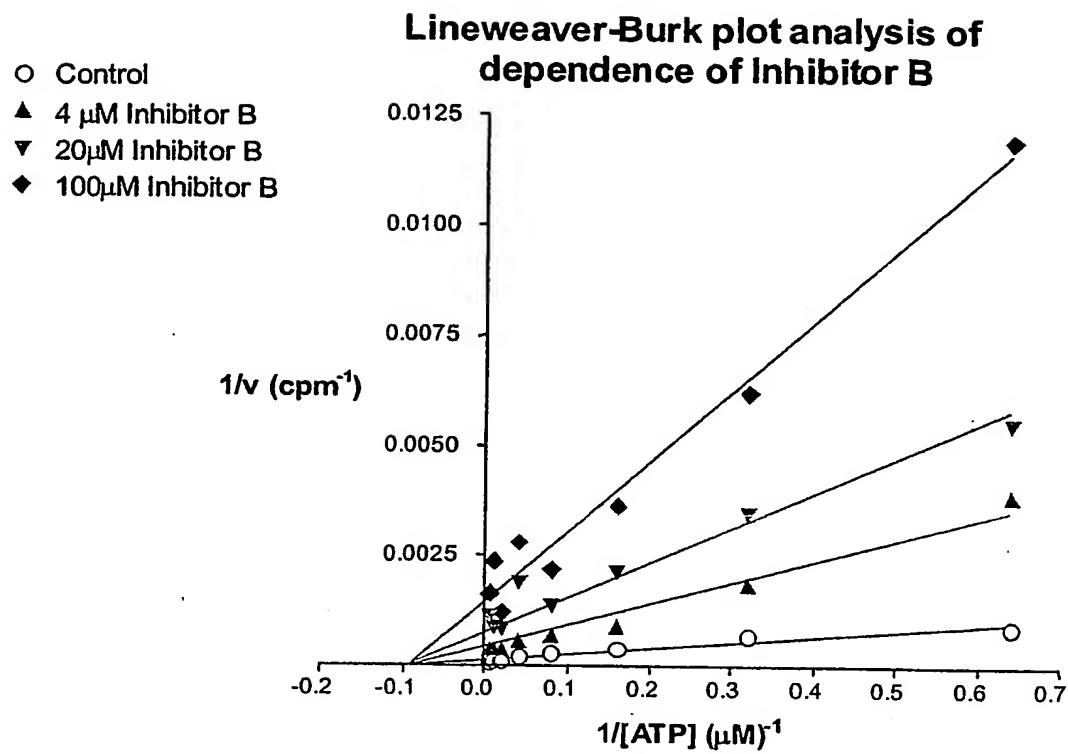
**FIGURE 11****FIGURE 12**

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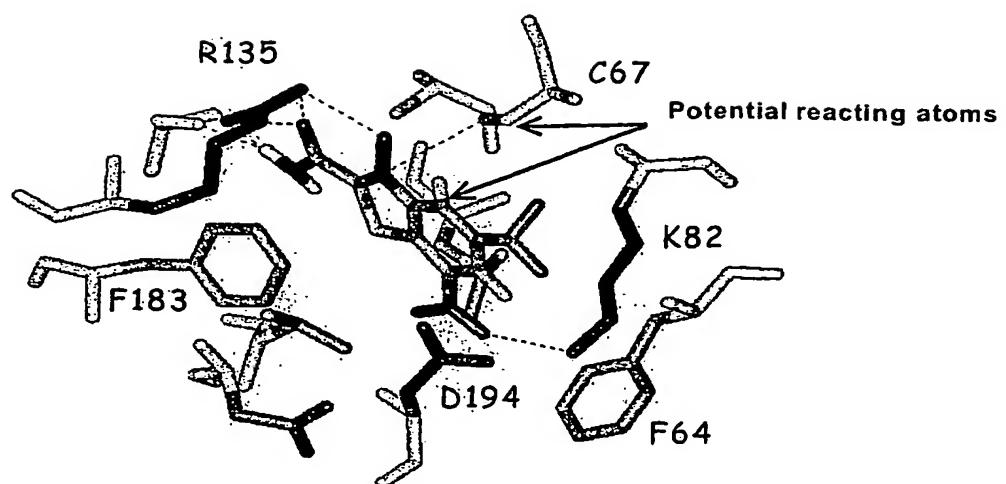
- Control
- ▲ 0.2 μ M Inhibitor A
- ▼ 0.4 μ M Inhibitor A
- ◆ 0.8 μ M Inhibitor A
- 1.6 μ M Inhibitor A

**FIGURE 13**

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**FIGURE 14**

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**FIGURE 15**

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